

0903

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/813,290

DATE: 09/10/2001
 TIME: 11:11:54

Input Set : A:\LEX-0151-USA SEQLIST.txt
 Output Set: N:\CRF3\09102001\I813290.raw

4 <110> APPLICANT: Walke, D. Wade
 5 Wilganowski, Nathaniel L.
 6 Turner, C. Alexander Jr.
 7 Hilbun, Erin
 8 Wang, Xiaoming
 9 Donoho, Gregory
 10 Scoville, John
 12 <120> TITLE OF INVENTION: Novel Human Secreted Proteins and Polynucleotides Encoding
 the Same

ENTERED

14 <130> FILE REFERENCE: LEX-0151-USA
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/813,290 ✓
 C--> 16 <141> CURRENT FILING DATE: 2001-03-20
 16 <150> PRIOR APPLICATION NUMBER: US 60/190,638
 17 <151> PRIOR FILING DATE: 2000-03-20
 19 <150> PRIOR APPLICATION NUMBER: US 60/191,188
 20 <151> PRIOR FILING DATE: 2000-03-22
 22 <150> PRIOR APPLICATION NUMBER: US 60/193,639
 23 <151> PRIOR FILING DATE: 2000-03-31
 25 <160> NUMBER OF SEQ ID NOS: 10
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 2628
 31 <212> TYPE: DNA
 32 <213> ORGANISM: homo sapiens
 34 <400> SEQUENCE: 1

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37 ctcccttcct cttccggccc tttcccgcc caggactggg ttggagccact gccttataag	180
38 ttgtggcttg gtggcagcag agcaaactac aaccggcggc cagcgggacc agagggcggc	240
39 tctgcaggca ggccggcagcg gtgccttcag ttcccccagca tgcccccctc ggcttggcc	300
40 atttgcgtgc tgcttaggggg cctcctgttc catggggta gctctggccc cagccccggc	360
41 cccagtgtgc cccgcctgctg gctctcctac cgagacctcc tttctgtccaa ccgcctctgcc	420
42 atctttctgg gcccccaagg ctccctgaac ctccaggcca ttgtacccataga tgagtaccga	480
43 gaccgcctct ttctgggtgg cctggacgccc ctctactctc tgccggctggaa ccaggcatgg	540
44 ccagatcccc gggaggctt gtggccaccc cagccaggac agagggagga gtgtgttcga	600
45 aagggaagag atcctttgac agagtgcgccc aacttctgtc ggtgtctaca gcctcacaac	660
46 cggaccacc tgcttagctg tgcaactggg gccttcaggc ccacctgtgc cctcatcaca	720
47 gttggccacc gtggggagca tttgtccac ctggaggctg gcaagtgtgg aagtggccgg	780
48 gggcggtgcc ctcacgagcc cagccgtccc tttgcccagca ctttcataga cggggagctg	840
49 tacacgggtc tcactgtga ctccctgggg cggaggccatg tttttcccg aagtggaggt	900
50 cctcgccag ctctgcgttc cggactctgac cagagtctct tgacgacc ccgggtttgtg	960
51 atggccccc ggttccatg gaaactctgac caggacaatg acaagggtta ctttttttttc	1020
52 tcggagacgg tcccttcgtcc cgtatgggtggc tggaaaccatg tcactgtcag ccgcgtggc	1080
53 cgcgtctgcg tgaatgtatgc tggggccag cgggtgtgg tggaaacaaatg gagcacttc	1140
54 ctcaggccca ggctggcttg ctgggtgccc gggccctgtg gtggccagac ccactttgac	1200
55 cagctagagg atgtgttcct gctgtggccc aaggccggga agagcctoga ggtgtacgctg	1260
56 ctgttcagca ccgtcagtgc cgtgttccag ggcttcggcc tctgtgtgtt ccacatggca	1320
57 gacatctggg aggtttcaa cggcccccattt gcccaccgag atggggctca gcaccagtgg	1380

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58	ggccctatg	ggggcaaggt	gccctccct	cgcctggcg	tgtccccag	caagatgacc	1440
59	gcacagccag	gacggcctt	tggcagcacc	aaggactacc	cagatgaggt	gctcagttt	1500
60	gcccggcccc	acccctcat	gttctggcct	gtgcggcctc	gacatggccg	ccctgtcctt	1560
61	gtcaagaccc	acctggccca	gcagctacac	cagatctgg	tggaccgcgt	ggaggcagag	1620
62	gatgggacct	acgatgtcat	tttcctgggg	actgactcag	ggtctgtgt	caaagtcatc	1680
63	gctctccagg	cagggggctc	agctgaacct	gaggaagtgg	ttctggagga	gctccagggt	1740
64	ttaagggtgc	caacacctat	caccgaaatg	gagatctctg	tcaaaaaggca	aatgtatac	1800
65	gtgggctctc	ggctgggtgt	ggcccgagctg	cggctgcacc	aatgtgagac	ttacggcact	1860
66	gcctgtgcag	agtgcgtcct	ggcccgggac	ccatactgtg	cctggatgg	tgccctctgt	1920
67	accactacc	gccccagcct	tggcaagcgc	cggttccgccc	ggcaggacat	ccggcacggc	1980
68	aaccctgccc	tgcagtgcct	gggccagagc	caggaagaag	aggcagtggtt	acttgtggca	2040
69	gccaccatgg	totacggcac	ggagcacaat	agcacattcc	tggagtgcct	gccaagtct	2100
70	ccccargctg	ctgtgcgtg	gctcttgcag	aggccagggg	atgagggggc	tgaccagggt	2160
71	aagacggacg	agcgagtctt	gcacacggag	cggggctgc	tgttccgcag	gcttagccgt	2220
72	ttcgatgcgg	gcacctacac	ctgcaccact	ctggagcatg	gcttctccca	gactgtggtc	2280
73	cgccctggcct	tggtgggtat	tgtggcctca	cagctggaca	acctgttccc	tccggagcca	2340
74	aagccagagg	agccccccagc	ccggggagggc	ctggcttcca	ccccacccaa	ggcctgttac	2400
75	aaggacatcc	tgcagctcat	tgcgttcgc	aacctgcccc	gggtggatga	gtactgtgag	2460
76	cgcgtgtgg	gcaggggcac	cacggaatgc	tcaggtgtct	tccggagccg	gagccggggc	2520
77	aagcaggcca	ggggcaagag	ctggcaggg	ctggagctag	gcaagaagat	gaagagccgg	2580
78	gtgcatgcgg	agcacaatcg	gacgccccgg	gaggtggagg	ccacgtag		2628
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81	<211>	LENGTH: 875					
82	<212>	TYPE: PRT					
83	<213>	ORGANISM: homo sapiens					
85	<400>	SEQUENCE: 2					
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88	Val Trp His Lys Ser Leu His Trp Ala Asn Lys Val Glu Gly Glu Ala						
89	20	25	30				
90	Ala Gly Gly Arg Gln Gly Pro Ser Leu Leu Leu Ser Ser Ala Pro Leu						
91	35	40	45				
92	Pro Ala Gln Asp Trp Val Glu Pro Leu Pro Tyr Lys Trp Trp Pro Gly						
93	50	55	60				
94	Gly Ser Arg Ala Asn Tyr Asn Arg Arg Pro Ala Gly Pro Glu Gly Gly						
95	65	70	75	80			
96	Ser Ala Gly Arg Arg Gln Arg Cys Pro Gln Phe Pro Ser Met Ala Pro						
97	85	90	95				
98	Ser Ala Trp Ala Ile Cys Trp Leu Leu Gly Gly Leu Leu Leu His Gly						
99	100	105	110				
100	Gly Ser Ser Gly Pro Ser Pro Gly Pro Ser Val Pro Arg Leu Arg Leu						
101	115	120	125				
102	Ser Tyr Arg Asp Leu Leu Ser Ala Asn Arg Ser Ala Ile Phe Leu Gly						
103	130	135	140				
104	Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp Glu Tyr Arg						
105	145	150	155	160			
106	Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser Leu Arg Leu						
107	165	170	175				
108	Asp Gln Ala Trp Pro Asp Pro Arg Glu Val Leu Trp Pro Pro Gln Pro						

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109	180	185	190
110 Gly Gln Arg Glu Glu Cys Val Arg Lys Gly Arg Asp Pro Leu Thr Glu			
111 195	200	205	
112 Cys Ala Asn Phe Val Arg Val Leu Gln Pro His Asn Arg Thr His Leu			
113 210	215	220	
114 Leu Ala Cys Gly Thr Gly Ala Phe Gln Pro Thr Cys Ala Leu Ile Thr			
115 225	230	235	240
116 Val Gly His Arg Gly Glu His Val Leu His Leu Glu Pro Gly Ser Val			
117 245	250	255	
118 Glu Ser Gly Arg Gly Arg Cys Pro His Glu Pro Ser Arg Pro Phe Ala			
119 260	265	270	
120 Ser Thr Phe Ile Asp Gly Glu Leu Tyr Thr Gly Leu Thr Ala Asp Phe			
121 275	280	285	
122 Leu Gly Arg Glu Ala Met Ile Phe Arg Ser Gly Gly Pro Arg Pro Ala			
123 290	295	300	
124 Leu Arg Ser Asp Ser Asp Gln Ser Leu Leu His Asp Pro Arg Phe Val			
125 305	310	315	320
126 Met Ala Ala Arg Ile Pro Glu Asn Ser Asp Gln Asp Asn Asp Lys Val			
127 325	330	335	
128 Tyr Phe Phe Ser Glu Thr Val Pro Ser Pro Asp Gly Gly Ser Asn			
129 340	345	350	
130 His Val Thr Val Ser Arg Val Gly Arg Val Cys Val Asn Asp Ala Gly			
131 355	360	365	
132 Gly Gln Arg Val Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala Arg			
133 370	375	380	
134 Leu Val Cys Ser Val Pro Gly Pro Gly Gly Ala Glu Thr His Phe Asp			
135 385	390	395	400
136 Gln Leu Glu Asp Val Phe Leu Leu Trp Pro Lys Ala Gly Lys Ser Leu			
137 405	410	415	
138 Glu Val Tyr Ala Leu Phe Ser Thr Val Ser Ala Val Phe Gln Gly Phe			
139 420	425	430	
140 Ala Val Cys Val Tyr His Met Ala Asp Ile Trp Glu Val Phe Asn Gly			
141 435	440	445	
142 Pro Phe Ala His Arg Asp Gly Pro Gln His Gln Trp Gly Pro Tyr Gly			
143 450	455	460	
144 Gly Lys Val Pro Phe Pro Arg Pro Gly Val Cys Pro Ser Lys Met Thr			
145 465	470	475	480
146 Ala Gln Pro Gly Arg Pro Phe. Gly Ser Thr Lys Asp Tyr Pro Asp Glu			
147 485	490	495	
148 Val Leu Gln Phe Ala Arg Ala His Pro Leu Met Phe Trp Pro Val Arg			
149 500	505	510	
150 Pro Arg His Gly Arg Pro Val Leu Val Lys Thr His Leu Ala Gln Gln			
151 515	520	525	
152 Leu His Gln Ile Val Val Asp Arg Val Glu Ala Glu Asp Gly Thr Tyr			
153 530	535	540	
154 Asp Val Ile Phe Leu Gly Thr Asp Ser Gly Ser Val Leu Lys Val Ile			
155 545	550	555	560
156 Ala Leu Gln Ala Gly Gly Ser Ala Glu Pro Glu Glu Val Val Leu Glu			
157 565	570	575	

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158 Glu Leu Gln Val Phe Lys Val Pro Thr Pro Ile Thr Glu Met Glu Ile
 159 580 585 590
 160 Ser Val Lys Arg Gln Met Leu Tyr Val Gly Ser Arg Leu Gly Val Ala
 161 595 600 605
 162 Gln Leu Arg Leu His Gln Cys Glu Thr Tyr Gly Thr Ala Cys Ala Glu
 163 610 615 620
 164 Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ala Ser Cys
 165 625 630 635 640
 166 Thr His Tyr Arg Pro Ser Leu Gly Lys Arg Arg Phe Arg Arg Gln Asp
 167 645 650 655
 168 Ile Arg His Gly Asn Pro Ala Leu Gln Cys Leu Gly Gln Ser Gln Glu
 169 660 665 670
 170 Glu Glu Ala Val Gly Leu Val Ala Ala Thr Met Val Tyr Gly Thr Glu
 171 675 680 685
 172 His Asn Ser Thr Phe Leu Glu Cys Leu Pro Lys Ser Pro Gln Ala Ala
 173 690 695 700
 174 Val Arg Trp Leu Leu Gln Arg Pro Gly Asp Glu Gly Pro Asp Gln Val
 175 705 710 715 720
 176 Lys Thr Asp Glu Arg Val Leu His Thr Glu Arg Gly Leu Leu Phe Arg
 177 725 730 735
 178 Arg Leu Ser Arg Phe Asp Ala Gly Thr Tyr Thr Cys Thr Thr Leu Glu
 179 740 745 750
 180 His Gly Phe Ser Gln Thr Val Val Arg Leu Ala Leu Val Val Ile Val
 181 755 760 765
 182 Ala Ser Gln Leu Asp Asn Leu Phe Pro Pro Glu Pro Lys Pro Glu Glu
 183 770 775 780
 184 Pro Pro Ala Arg Gly Leu Ala Ser Thr Pro Pro Lys Ala Trp Tyr
 185 785 790 795 800
 186 Lys Asp Ile Leu Gln Leu Ile Gly Phe Ala Asn Leu Pro Arg Val Asp
 187 805 810 815
 188 Glu Tyr Cys Glu Arg Val Trp Cys Arg Gly Thr Thr Glu Cys Ser Gly
 189 820 825 830
 190 Cys Phe Arg Ser Arg Ser Arg Gly Lys Gln Ala Arg Gly Lys Ser Trp
 191 835 840 845
 192 Ala Gly Leu Glu Leu Gly Lys Lys Met Lys Ser Arg Val His Ala Glu
 193 850 855 860
 194 His Asn Arg Thr Pro Arg Glu Val Glu Ala Thr
 195 865 870 875
 197 <210> SEQ ID NO: 3
 198 <211> LENGTH: 2349
 199 <212> TYPE: DNA
 200 <213> ORGANISM: homo sapiens
 202 <400> SEQUENCE: 3
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 205 ctgtctgcca accgcctctgc catctttctg ggcccccagg gctccctgaa cctccaggcc 180
 206 atgtacctag atgagtaaccg agaccgcctc tttctgggtg gcctggacgc cctctactct 240
 207 ctgcggctgg accaggcatg gccagatccc cgggaggtcc tgtggccacc gcagccagga 300
 208 cagagggagg agtgtgttcg aaagggaga gatcccttga cagagtgcgc caacttcgtg 360

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Output Set: N:\CRF3\09102001\I813290.raw

209	cgggtgctac	agcctcacaa	ccggaccac	ctgcttagcct	gtggactgg	ggccttccag	420
210	cccacctgtg	ccctcatcac	agttggccac	cgtggggagc	atgtgtcca	cctggagcct	480
211	ggcagtgtgg	aaagtggccg	ggggcggtgc	cctcacgagc	ccagccgtcc	cttgccagc	540
212	accttcata	acggggagct	gtacacgggt	ctcaactgctg	acttcctggg	gcgagaggcc	600
213	atgatcttcc	gaagtggagg	tcctcgccca	gctctgcgtt	cogactctga	ccagagtctc	660
214	ttgcacgacc	cccggtttgt	gatggccgcc	cgatccctg	agaactctga	ccaggacaat	720
215	gacaagggt	acttcttctt	ctcgagacg	gtccccctgc	ccgatggtgg	ctcgaaccat	780
216	gtcaactgtca	gccgcgtggg	ccgcgtctgc	gtaaatgatg	ctgggggcca	gcgggtgctg	840
217	gtgaacaaaat	ggagcactt	cctcaaggcc	aggctggtct	gctcggtgcc	cggcccttgtt	900
218	gggtccgaga	cccaacttga	ccagctagag	gatgtgttcc	tgctgtggcc	caaggccggg	960
219	aagagctcg	agggtacgc	gctgttcagc	accgtca	ccgtgttcca	gggcttcgccc	1020
220	gtctgtgtgt	accacatggc	agacatctgg	gagttttca	acgggcctt	tgcaccacgaa	1080
221	gatgggcctc	agcaccagt	ggggccctat	ggggcaagg	tgcccttccc	tcgccttggc	1140
222	gtgtgccccca	gcaagatgac	cgcacagcc	ggacggcctt	ttggcagcac	caaggactac	1200
223	ccagatgagg	tgctgcagtt	tgcccagcc	cacccctca	tgttctgccc	tgtcgccct	1260
224	cgacatggcc	gccctgtct	tgtcaagacc	cacccggcc	agcagctaca	ccagatcgta	1320
225	gtggaccgcg	tggaggcaga	ggatgggacc	tacgatgtca	ttttcctggg	gactgactca	1380
226	gggtctgtgc	tcaaagtcat	cgctctccag	gcagggggct	cagctgaacc	tgaggaagtg	1440
227	gttctggagg	agctccaggt	gtttaagggt	ccaacaccta	tcaccgaaat	ggagatctct	1500
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229	caatgtgaga	cttacggcac	tgcctgtgca	gagtgtgcc	tggcccccggg	cccatactgt	1620
230	gcctgggatg	gtgcctctg	tacccactac	cgcccccagcc	ttggcaagcg	ccgggtccgc	1680
231	ccgcaggaca	tccggcacgg	caaccctgccc	ctgcagtgcc	tggcccaagag	ccaggaagaa	1740
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233	ctggagtgcc	tgcccaagtc	tccccargt	gctgtgcgt	ggcttgc	gaggccaggg	1860
234	gatgaggggc	ctgaccaggt	gaagacggac	gagcagatct	tgcacacgg	gcgggggctg	1920
235	ctgttccgca	ggcttagccg	tttcgatgccc	ggcacctaca	cctgcaccac	tctggagcat	1980
236	ggcttctccc	agactgtgg	ccgcctggct	ctgggtgtg	ttgtggcctc	acagctggac	2040
237	aacctgttcc	ctccggagcc	aaagccagag	gagcccccag	cccgggggagg	cctggcttcc	2100
238	accccacca	aggctggta	caaggacatc	ctgcagctca	ttggcttgc	caacactgccc	2160
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240	ttccggagcc	ggagccgggg	caagcaggcc	aggggcaaga	gctggcagg	gctggagcta	2280
241	ggcaagaaga	tgaagagccg	ggtgcattcc	gagcacaatc	ggacccccg	ggaggtggag	2340
242	gccacgtag						2349

244 <210> SEQ ID NO: 4

245 <211> LENGTH: 782

246 <212> TYPE: PRT

247 <213> ORGANISM: homo sapiens

249 <400> SEQUENCE: 4

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252 Leu His Gly Gly Ser Ser Gly Pro Ser Pro Gly Pro Ser Val Pro Arg

253 20 25 30

254 Leu Arg Leu Ser Tyr Arg Asp Leu Leu Ser Ala Asn Arg Ser Ala Ile

255 35 40 45

256 Phe Leu Gly Pro Gln Gly Ser Leu Asn Leu Gln Ala Met Tyr Leu Asp

257 50 55 60

258 Glu Tyr Arg Asp Arg Leu Phe Leu Gly Gly Leu Asp Ala Leu Tyr Ser

259 65 70 75 80

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7